

Appendix III

Alignment of SEQ ID NO: 1479 of Tang et al with the sequence of GenBank Accession No. BAA23691.2

>BAA23691.2 KIAA0395 [Homo sapiens]
Length=879

Score = 1827 bits (4732), Expect = 0.0, Method: Compositional matrix adjust.
Identities = 877/879 (99%), Positives = 878/879 (99%), Gaps = 0/879 (0%)

Query	78	SCKYCDFRSHDMTQFVGHMNSHTDFNKDPTFVCSGCSFLAKTPEGLSLHNATCHSGEAS	137
Sbjct	1	SCKYCDFRSHDMTQFVGHMNSHTDFNKDPTFVCSGCSFLAKTPEGLSLHNATCHSGEAS	60
Query	138	FVWNVAKPDNHVVVEQSIPESTSTPDLAGEPSAEGADGQAEIIITKTPIMKIMKGKAAK	197
Sbjct	61	FVWNVAKPDNHVVVEQSIPESTSTPDLAGEPSAEGADGQAEIIITKTPIMKIMKGKAAK	120
Query	198	KIHITLKENVPSQPVGEALPKLSTGEMEVREGDHSFINGAVPVVSQASASSAKNPHAANGPL	257
Sbjct	121	KIHITLKENVPSQPVGEALPKLSTGEMEVREGDHSFINGAVPVVSQASASSAKNPHAANGPL	180
Query	258	IGTVFVLPAGIAQFLSLQQQPPVHAQHNVHQPLPTAKALPKVMIPLSSIPTYAAMDSNS	317
Sbjct	181	IGTVFVLPAGIAQFLSLQQQPPVHAQHNVHQPLPTAKALPKVMIPLSSIPTYAAMDSNS	240
Query	318	FLKNSFHKKFPYPTKAELCYLTVVTKYPPEEQKIMWFTAQRLKQGISWSPEEIEDARKKMFN	377
Sbjct	241	FLKNSFHKKFPYPTKAELCYLTVVTKYPPEEQKIMWFTAQRLKQGISWSPEEIEDARKKMFN	300
Query	378	TVIQSVFPQFTITVLENTPLVASAGNVQHLIQAAALPGHVVGQPEGTGGGLLVTPQLMANGLO	437
Sbjct	301	TVIQSVFPQFTITVLENTPLVASAGNVQHLIQAAALPGHVVGQPEGTGGGLLVTPQLMANGLO	360
Query	438	ATSSFLPLTVTSVPKQPGVAPINTVCSNTTSAVKVVMNAQSLLTACPSITSQAFLDASIY	497
Sbjct	361	ATSSFLPLTVTSVPKQPGVAPINTVCSNTTSAVKVVMNAQSLLTACPSITSQAFLDASIY	420
Query	498	KNKKSHEQLSALKGSFCRNQFFGQSEVEHLTKVTGLSTREVRKWFSDRRYHCRNLKGSRA	557
Sbjct	421	KNKKSHEQLSALKGSFCRNQFFGQSEVEHLTKVTGLSTREVRKWFSDRRYHCRNLKGSRA	480
Query	558	MIPGDHSSIIIDSVPEVSFSPSSKVPVETCIPPTATLATHPSAKRQSWHQTPDFTPTKYK	617
Sbjct	481	MIPGDHSSIIIDSVPEVSFSPSSKVPVETCIPPTATLATHPSAKRQSWHQTPDFTPTKYK	540
Query	618	ERAPQLRALESSFAQNPLPLDEELDRLRSETKMTREIDSWFSERRKKNVNAEETKAAE	677
Sbjct	541	ERAPQLRALESSFAQNPLPLDEELDRLRSETKMTREIDSWFSERRKKNVNAEETKAAE	600
Query	678	NASQEEEEAAEDEGGEEDLASELRVSGENGSLMPSSHILAEKRVSPKINLKNLRVTEA	737
Sbjct	601	NASQEEEEAAEDEGGEEDLASELRVSGENGSLMPSSHILAEKRVSPKINLKNLRVTEA	660
Query	738	NGRNEIPGLGACDPEDDESINKLAELPGKVSCKKTAQQRHLLRQLFVQTQWPSNQYDSI	797
Sbjct	661	NGRNEIPGLGACDPEDDESINKLAELPGKVSCKKTAQQRHLLRQLFVQTQWPSNQYDSI	720
Query	798	MAQTGLPRPEVVRWFGDSRYALKNGQLKWYEDYKRGNFPPGLLVIAFGNRELLQDYMTM	857
Sbjct	721	MAQTGLPRPEVVRWFGDSRYALKNGQLKWYEDYKRGNFPPGLLVIAFGNRELLQDYMTM	780
Query	858	KMLYEEDLQNLCDKTQMSQQVKQWFAEKMGEETRAVADTGSSEDQGPGETTAVHKGGMG	917
Sbjct	781	KMLYEEDLQNLCDKTQMSQQVKQWFAEKMGEETRAVADTGSSEDQGPGETTAVHKGGMG	840
Query	918	DTYSEVSENSESWEPRVPEASSEPFDTSSPQAGRQLETD	956
Sbjct	841	DTYSEVSENSESWEPRVPEASSEPFDTSSPQAGRQLETD	879